

# SEQUENCE LISTING

<110> Harrington, et al.

<120> Mammalian Flap Specific-Endonuclease

<130> 9584-017

<140> 09/586,744

<141> 2000-06-02

<160> 74

<170> PatentIn version 3.0

<210> 1

<211> 380

<212> PRT

<213> Artificial

<220>

<223> Peptide

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Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu	85	90	95	
Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln	100	105	110	
Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gly	Glu	Val	Glu	Lys	Phe	Thr	Lys	115	120	125	
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu	130	135	140	
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu	145	150	155	160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala	165	170	175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg	180	185	190	
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His	195	200	205	
Leu	Ser	Arg	Ile	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val	210	215	220	
Asp	Leu	Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly	225	230	235	240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile	245	250	255	
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Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val	275	280	285	
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu	290	295	300	
Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg	305	310	315	320
Ile	Arg	Ser	Gly	Val	Lys	Arg	Leu	Ser	Lys	Ser	Arg	Gln	Gly	Ser	Thr	325	330	335	
Gln	Gly	Arg	Leu	Asp	Asp	Phe	Phe	Lys	Val	Thr	Gly	Ser	Leu	Ser	Ser	340	345	350	
Ala	Lys	Arg	Lys	Glu	Pro	Glu	Pro	Lys	Gly	Ser	Thr	Lys	Lys	Lys	Ala	355	360	365	

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accagccacc tgatggggcat gttctaccgc accattcgca tgatggagaa cggcatacaag	240
cccgtgtatg tctttgatgg caagccgcca cagctcaagt caggcgagct ggccaaacgc	300
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caggaggttg aaaaattcac taagcggctg gtgaaggctc ctaagcagca caatgatgag	420
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Ile	Asp	Ala	Ser	Met	Ser	Ile	Tyr	Gln	Phe	Leu	Ile	Ala	Val	Arg	Gln	35	40	45	
Gly	Gly	Asp	Val	Leu	Gln	Asn	Glu	Glu	Gly	Glu	Thr	Thr	Ser	Leu	Met	50	55	60	
Gly	Met	Phe	Tyr	Arg	Thr	Ile	Arg	Met	Glu	Asn	Gly	Ile	Lys	Pro	Val	65	70	75	80
Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu	Leu	Ala	85	90	95	
Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln	Gln	Ala	100	105	110	
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Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Ser	Cys	145	150	155	160
Ala	Ala	Leu	Ala	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala	Thr	Glu	Asp	165	170	175	
Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg	His	Leu	Thr	180	185	190	
Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His	Leu	Ser	Arg	195	200	205	
Val	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val	Asp	Leu	Cys	210	215	220	

Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly	Ile	Gly	Ala	
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				245					250					255		
Val	Arg	Arg	Leu	Asp	Pro	Ser	Lys	Tyr	Pro	Val	Pro	Glu	Asn	Trp	Leu	
			260					265					270			
His	Lys	Glu	Ala	Gln	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val	Val	Asp	Pro	
		275					280					285				
Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu	Glu	Leu	Val	
	290					295					300					
Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg	Ile	Arg	Ser	
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Gly	Val	Lys	Arg	Leu	Ser	Lys	Ser	Arg	Gln	Gly	Ser	Thr	Gln	Gly	Arg	
				325					330					335		
Leu	Asp	Asp	Phe	Phe	Lys	Val	Thr	Gly	Ser	Leu	Ser	Ser	Ala	Lys	Arg	
			340					345					350			
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gaagaagagt tgggtcaaatt tatgtgtggt gaaaagcagt tttctgaaga gcgaattcgc	960
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35 40 45

Gln Asp Gly Gly Gln Leu Thr Asn Glu Ala Gly Glu Thr Thr Ser His  
50 55 60

Leu Met Gly Met Phe Tyr Arg Thr Leu Arg Met Ile Asp Asn Gly Ile  
65 70 75 80

Lys Pro Cys Tyr Val Phe Asp Gly Lys Pro Pro Asp Leu Lys Ser His  
85 90 95

Glu Leu Thr Lys Arg Ser Ser Arg Arg Val Glu Thr Glu Lys Lys Leu  
100 105 110

Ala Glu Ala Thr Thr Glu Leu Glu Lys Met Lys Gln Glu Arg Arg Leu  
115 120 125

Val Lys Val Ser Lys Glu His Asn Glu Glu Ala Gln Lys Leu Leu Gly  
130 135 140

Leu Met Gly Ile Pro Tyr Ile Ile Ala Pro Thr Glu Ala Glu Ala Gln  
145 150 155 160

Cys Ala Glu Leu Ala Lys Lys Gly Lys Val Tyr Ala Ala Ala Ser Glu  
165 170 175

Asp Met Asp Thr Leu Cys Tyr Arg Thr Pro Phe Leu Leu Arg His Leu  
180 185 190

Thr Phe Ser Glu Ala Lys Lys Glu Pro Ile His Glu Ile Asp Thr Glu  
195 200 205

Leu Val Leu Arg Gly Leu Asp Leu Thr Ile Glu Gln Phe Val Asp Leu  
210 215 220

Cys Ile Met Leu Gly Cys Asp Tyr Cys Glu Ser Ile Arg Gly Val Gly  
225 230 235 240

Pro Val Thr Ala Leu Lys Leu Ile Lys Thr His Gly Ser Ile Glu Lys  
245 250 255

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Pro	Glu	Val	Ile	Asp	Gly	Asn	Glu	Ile	Asn	Leu	Lys	Trp	Ser	Pro	Pro	
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Lys	Glu	Lys	Glu	Leu	Ile	Glu	Tyr	Leu	Cys	Asp	Asp	Lys	Lys	Phe	Ser	
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Glu	Glu	Arg	Val	Lys	Ser	Gly	Ile	Ser	Arg	Leu	Lys	Lys	Gly	Leu	Lys	
				325					330					335		
Ser	Gly	Ile	Gln	Gly	Arg	Leu	Asp	Gly	Phe	Phe	Gln	Val	Val	Pro	Lys	
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Thr	Lys	Glu	Gln	Leu	Ala	Ala	Ala	Ala	Lys	Arg	Ala	Gln	Glu	Asn	Lys	
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acaacgtcac acttgatggg tatgttttat aggacactga gaatgattga taacggtatc	240
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tgtgctgagt tggcaaagaa gggaaagggt tatgccgcag caagtgaaga tatggacaca	540
ctctgttata gaacaccctt cttgttgaga catttgactt tttcagaggc caagaaggaa	600



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Ile	Trp	Ile	Tyr	Gln	Phe	Leu	Lys	Ala	Val	Arg	Asp	Gln	Glu	Gly	Asn
		35					40					45			
Ala	Val	Lys	Asn	Ser	His	Ile	Thr	Gly	Phe	Phe	Arg	Arg	Ile	Cys	Lys
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Leu	Leu	Tyr	Phe	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	Gly	Gly	Val
65					70					75					80
Pro	Val	Leu	Lys	Arg	Glu	Thr	Ile	Arg	Gln	Arg	Lys	Glu	Arg	Arg	Gln
			85						90					95	
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<212> DNA

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gttaataaac gcaaaaagaa ggggaagcaa aaaaggatta atgaattttt tccaaggag      1080
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                                     Met Glu Ile His
                                     1

ggc ctt gcc aaa cta att gct gat gtg gcc ccc agt gcc atc cgt gag      163
Gly Leu Ala Lys Leu Ile Ala Asp Val Ala Pro Ser Ala Ile Arg Glu
5                               10                               15                               20

aat gac atc aag agc tac ttt ggt cgc aaa gtg gcc atc gat gcc tcc      211
Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala Ile Asp Ala Ser
                               25                               30                               35

atg agc atc tac cag ttc ctg att gct gtt cgt cag ggt ggg gat gtg      259
Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln Gly Gly Asp Val
                               40                               45                               50

ctg cag aac gag gag ggt gag acc acc agc ctg atg ggc atg ttc tac      307
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                               55                               60                               65

cgt acc atg cgc atg gag aat ggc atc aag cct gtg tac gtc ttt gat      355
Arg Thr Met Arg Met Glu Asn Gly Ile Lys Pro Val Tyr Val Phe Asp
                               70                               75                               80

ggc aaa cca cca cag ctg aag tca ggc gag ctg gcc aag cgc agt gag      403
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85                               90                               95                               100

agg cgc gcc gag gct gag aag caa ctg cag cag gct cag cag gct ggg      451
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                               105                               110                               115

atg gag gag gag gtg gag aag ttc acc aag agg ctc gtg aag gtc acc      499
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                               120                               125                               130

aag caa cac aat gat gag tgc aaa cac ctg ctg agc ctc atg ggc atc      547
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ctc act ttt ggc agc ccc gtg cta atg cga cac tta act gcc agt gag Leu Thr Phe Gly Ser Pro Val Leu Met Arg His Leu Thr Ala Ser Glu 185 190 195	691
gcc aag aag ctg ccc atc caa gag ttc cat ctg agc cgc gtc ctg cag Ala Lys Lys Leu Pro Ile Gln Glu Phe His Leu Ser Arg Val Leu Gln 200 205 210	739
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ctg gac ccc agc aag tac ccc gtt cca gag aac tgg ctc cac aag gaa Leu Asp Pro Ser Lys Tyr Pro Val Pro Glu Asn Trp Leu His Lys Glu 265 270 275	931
gcc cag cag ctc ttc ctg gag cca gaa gta gtg gac cca gag tct gtg Ala Gln Gln Leu Phe Leu Glu Pro Glu Val Val Asp Pro Glu Ser Val 280 285 290	979
gag ctg aag tgg agc gag cca aat gaa gaa gag ttg gtc aaa ttt atg Glu Leu Lys Trp Ser Glu Pro Asn Glu Glu Glu Leu Val Lys Phe Met 295 300 305	1027
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gaa ccc aag ggg cct gct aag aag aaa gca aag act ggg gga gcg ggg Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr Gly Gly Ala Gly 360 365 370	1219
aag ttc cga agg gga aaa taaacctgtc cttccctccc actgtccttg Lys Phe Arg Arg Gly Lys	1267

375

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accccaggct gtctatctgt tttgtaccct cggctgcagc acatccctct tgtccctcgt 1327
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Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
20           25           30

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Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
35           40           45

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Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser Leu Met
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Gly	Met	Phe	Tyr	Arg	Thr	Met	Arg	Met	Glu	Asn	Gly	Ile	Lys	Pro	Val	65	70	75	80
Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu	Leu	Ala	85	90	95	
Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln	Gln	Ala	100	105	110	
Gln	Gln	Ala	Gly	Met	Glu	Glu	Glu	Val	Glu	Lys	Phe	Thr	Lys	Arg	Leu	115	120	125	
Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu	Leu	Ser	130	135	140	
Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Ser	145	150	155	160
Cys	Ala	Ala	Leu	Ala	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala	Thr	Glu	165	170	175	
Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg	His	Leu	180	185	190	
Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His	Leu	Ser	195	200	205	
Arg	Val	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val	Asp	Leu	210	215	220	
Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly	Ile	Gly	225	230	235	240
Ala	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile	Glu	Glu	245	250	255	
Ile	Val	Arg	Arg	Leu	Asp	Pro	Ser	Lys	Tyr	Pro	Val	Pro	Glu	Asn	Trp	260	265	270	
Leu	His	Lys	Glu	Ala	Gln	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val	Val	Asp	275	280	285	
Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu	Glu	Leu	290	295	300	

Val Lys Phe Met Cys Gly Glu Lys Gln Phe Phe Glu Glu Arg Ile Arg  
 305 310 315 320

Ser Gly Val Lys Arg Leu Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly  
 325 330 335

Arg Leu Asp Asp Phe Phe Lys Val Thr Gly Ser Leu Ser Ser Ala Lys  
 340 345 350

Arg Lys Glu Pro Glu Pro Lys Gly Pro Ala Lys Lys Lys Ala Lys Thr  
 355 360 365

Gly Gly Ala Gly Lys Phe Arg Arg Gly Lys  
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Arg Glu Asn Asp Ile Lys  
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Glu Gln Glu Val Glu Lys Phe Thr Lys Arg Leu Val Lys Val Thr Lys  
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Gln His Asn Asp  
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<210> 21

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1 5 10 15

Ala Lys Lys Leu Pro Ile Gln  
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Ile Leu Leu Gly Ser  
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Ser Ile Glu Glu Ile Val Arg Arg  
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Pro Glu Asn Trp Leu His Lys Glu Ala His Gln Leu Phe Leu Glu Pro  
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Glu Val Leu Asp  
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<212> PRT

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<400> 25

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Lys Gln Phe Ser Glu Glu  
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Ser Lys Ser Arg Gln Gly Ser Thr Gln Gly Arg Leu Asp Asp Phe Phe  
 1 5 10 15

Lys Val Thr Gly Ser Leu  
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<210> 27

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cagttcctga ttgctgttcg ccagggtggg gatgtgctgc agaattgagga gggtgagacc	180
accagccacc tgatgggcat gttctaccgc accattcgca tgatggagaa cggcatacaag	240
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caggaggtgg aaaaattcac taagcggctg gtgaaggtca ctaagcagca caatgatgag	420
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gatgatttct tcaaggtgac cggctcactc tcttcagcta agcgcaagga gccagaaccc	1080
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